

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/573,131

Source: IFWP

Date Processed by STIC: 4/4/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/04/2006

PATENT APPLICATION: US/10/573,131

TIME: 10:32:39

Input Set : A:\5470.401WO.ST25.txt

Output Set: N:\CRF4\04042006\J573131.raw

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3 <110> APPLICANT: University of North Carolina-Chapel Hill
4   Stafford, Darrel
5   Li, Tao
7 <120> TITLE OF INVENTION: IDENTIFICATION OF THE GENE FOR VITAMIN K EPOXIDE REDUCTASE
9 <130> FILE REFERENCE: 5470.401WO
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/573,131
C--> 11 <141> CURRENT FILING DATE: 2006-03-23
11 <150> PRIOR APPLICATION NUMBER: US 60/505,527
12 <151> PRIOR FILING DATE: 2003-09-23
14 <160> NUMBER OF SEQ ID NOS: 34
16 <170> SOFTWARE: PatentIn version 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 21
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial sequence
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24 <223> OTHER INFORMATION: Synthetic oligonucleotide primer
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33 <213> ORGANISM: Artificial sequence
35 <220> FEATURE:
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240 ttcttagatc aatca 3915
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 806

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246 <213> ORGANISM: Homo sapiens
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250 <221> NAME/KEY: CDS
251 <222> LOCATION: (48)..(536)
253 <400> SEQUENCE: 9
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255                                     Met Gly Ser
256                                     1
258 acc tgg ggg agc cct ggc tgg gtg cgg ctc gct ctt tgc ctg acg ggc      104
259 Thr Trp Gly Ser Pro Gly Trp Val Arg Leu Ala Leu Cys Leu Thr Gly
260      5              10              15
262 tta gtg ctc tcg ctc tac gcg ctg cac gtg aag gcg gcg cgc gcc cgg      152
263 Leu Val Leu Ser Leu Tyr Ala Leu His Val Lys Ala Ala Arg Ala Arg
264 20              25              30              35
266 gac cgg gat tac cgc gcg ctc tgc gac gtg ggc acc gcc atc agc tgt      200
267 Asp Arg Asp Tyr Arg Ala Leu Cys Asp Val Gly Thr Ala Ile Ser Cys
268      40              45              50
270 tgc cgg ttc ttc tgc tgc agg tgg ggc agg ggt ttc ggg ctg ggc gag      248
271 Ser Arg Val Phe Ser Ser Arg Trp Gly Arg Gly Phe Gly Leu Val Glu
272      55              60              65
274 cat gtg ctg gga cag gac agc atc ctc aat caa tcc aac agc ata ttc      296
275 His Val Leu Gly Gln Asp Ser Ile Leu Asn Gln Ser Asn Ser Ile Phe
276      70              75              80
278 ggt tgc atc ttc tac aca cta cag cta ttg tta ggt tgc ctg cgg aca      344
279 Gly Cys Ile Phe Tyr Thr Leu Gln Leu Leu Leu Gly Cys Leu Arg Thr
280      85              90              95
282 cgc tgg gcc tct gtc ctg atg ctg ctg agc tcc ctg gtg tct ctc gct      392
283 Arg Trp Ala Ser Val Leu Met Leu Leu Ser Ser Leu Val Ser Leu Ala
284 100              105              110              115
286 ggt tct gtc tac ctg gcc tgg atc ctg ttc ttc gtg ctc tat gat ttc      440
287 Gly Ser Val Tyr Leu Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe
288      120              125              130
290 tgc att gtt tgt atc acc acc tat gct atc aac gtg agc ctg atg tgg      488
291 Cys Ile Val Cys Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp
292      135              140              145
294 ctc agt ttc cgg aag gtc caa gaa ccc cag ggc aag gct aag agg cac      536
295 Leu Ser Phe Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His
296      150              155              160
298 tgagccctca acccaagcca ggctgacctc atctgctttg ctttggcatg tgagccttgc      596
300 ctaagggggc atatctgggt ccctagaagg ccctagatgt ggggcttcta gattaccccc      656
302 tcctcctgcc ataccgcac atgacaatgg accaaatgtg ccacacgctc gctctttttt      716
304 acacccagtg cctctgactc tgtccccatg ggctgggtctc caaagctctt tccattgccc      776
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311 <212> TYPE: PRT
312 <213> ORGANISM: Homo sapiens
314 <400> SEQUENCE: 10

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 317 1 5 10 15
 320 Leu Thr Gly Leu Val Leu Ser Leu Tyr Ala Leu His Val Lys Ala Ala
 321 20 25 30
 324 Arg Ala Arg Asp Arg Asp Tyr Arg Ala Leu Cys Asp Val Gly Thr Ala
 325 35 40 45
 328 Ile Ser Cys Ser Arg Val Phe Ser Ser Arg Trp Gly Arg Gly Phe Gly
 329 50 55 60
 332 Leu Val Glu His Val Leu Gly Gln Asp Ser Ile Leu Asn Gln Ser Asn
 333 65 70 75 80
 336 Ser Ile Phe Gly Cys Ile Phe Tyr Thr Leu Gln Leu Leu Leu Gly Cys
 337 85 90 95
 340 Leu Arg Thr Arg Trp Ala Ser Val Leu Met Leu Leu Ser Ser Leu Val
 341 100 105 110
 344 Ser Leu Ala Gly Ser Val Tyr Leu Ala Trp Ile Leu Phe Phe Val Leu
 345 115 120 125
 348 Tyr Asp Phe Cys Ile Val Cys Ile Thr Thr Tyr Ala Ile Asn Val Ser
 349 130 135 140
 352 Leu Met Trp Leu Ser Phe Arg Lys Val Gln Glu Pro Gln Gly Lys Ala
 353 145 150 155 160

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362 <212> TYPE: DNA

363 <213> ORGANISM: Homo sapiens

365 <400> SEQUENCE: 11

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 370 agaggttagg atactgtcaa ggggtgtgtgt ggccaaagga gtggttctgt gaatgtatgg 180
 372 gagaaaggga gaccgaccac caggaagcac tgggtgaggca ggaccgcgga ggatgggagg 240
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 378 acaacaggac ttggcatagg gtaagcgcaa atgctgttaa ccacactaac acactttttt 420
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 392 aactcccatc atgcctggca gccgctgggg ccgcgattcc gcacgtccct taccgcgttc 840
 394 actagtcccg gcattcttcg ctgttttccct aactcgcccg cttgactagc gccctggaac 900
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date